

Amendments to the Claims

Please cancel all presently pending claims without prejudice. Please add new claims 21-35 as shown below in the List of Claims.

List of Claims

1-20. Cancelled

21. (New) A process for the production of an L-amino acid comprising:
- a) culturing a recombinant microorganism from the Enterobacteriaceae family in a fermentation medium, wherein;
 - i) said recombinant microorganism produces said L-amino acid;
 - ii) said recombinant microorganism has been transformed with a vector comprising an open reading frame (ORF) that encodes a protein comprising the amino acid sequence of SEQ ID NO:4;
 - iii) said ORF is overexpressed in said recombinant microorganism by increasing the copy number of said ORF or by linking said ORF to a promoter;
 - b) allowing said fermentation medium or said recombinant microorganism to become enriched in said L-amino acid; and
 - b) isolating said L-amino acid.
22. (New) The process of claim 21, wherein said ORF encodes protein that consists of the amino acid sequence of SEQ ID NO:4
23. (New) The process of claim 21 wherein some or all of the constituents of said fermentation medium and/or the biomass of said recombinant microorganism are isolated with said L-amino acid.
24. (New) The process of claim 21 wherein said ORF that encodes a protein with the amino acid sequence of SEQ ID NO:4 comprises the nucleotide sequence of SEQ ID NO:3.

25. (New) The process of claim 24 wherein said ORF that encodes a protein with the amino acid sequence of SEQ ID NO:4 consists of the nucleotide sequence of SEQ ID NO:3.
26. (New) The process of claim 21, wherein the genus of said recombinant microorganism is selected from the group consisting of: *Escherichia*; *Erwinia*; *Providencia*; and *Serratia*.
27. (New) The process of claim 21, wherein said microorganism overexpresses said ORF and, in addition, the activity of one or more additional genes is overexpressed, said one or more additional genes being selected from the group consisting of:
- a) the thrABC operon coding for aspartate kinase, homoserine dehydrogenase, homoserine kinase and threonine synthase;
 - b) the pyc gene coding for pyruvate carboxylase;
 - c) the pps gene for phosphoenolpyruvate synthase;
 - d) the ppc gene coding for phosphoenolpyruvate carboxylase;
 - e) the genes pntA and pntB coding for transhydrogenase;
 - f) the rhtB gene imparting homoserine resistance;
 - g) the mqo gene coding for malate:quinone oxidoreductase;
 - h) the rhtC gene imparting threonine resistance;
 - i) the thrE gene coding for the threonine-export protein;
 - j) the gdhA gene coding for glutamate dehydrogenase;
 - k) the hns gene coding for the DNA binding protein HLP-II;
 - l) the pgm gene coding for phosphoglucomutase;
 - m) the fba gene coding for fructose biphosphate aldolase;
 - n) the ptsH gene coding for phosphohistidine protein hexose phosphotransferase;
 - o) the ptsI gene coding for enzyme I of the phosphotransferase system;
 - p) the crr gene coding for the glucose-specific IIA component;
 - q) the ptsG gene coding for the glucose-specific IIBC component;
 - r) the lrp gene coding for the regulator of the leucine regulon;
 - s) the csrA gene coding for the global regulator Csr;
 - t) the fadR gene coding for the regulator of the fad regulon;

- u) the *iclR* gene coding for the regulator of central intermediary metabolism;
- v) the *mopB* gene coding for the 10 kDa chaperon;
- w) the *ahpC* gene coding for the small subunit of alkyl hydroperoxide reductase;
- x) the *ahpF* gene coding for the large subunit of alkyl hydroperoxide reductase;
- y) the *cysK* gene coding for cysteine synthase A;
- z) the *cysB* gene coding for the regulator of the *cys* regulon;
- aa) the *cysJ* gene coding for the flavoprotein of NADPH sulfite reductase;
- bb) the *cysI* gene coding for the haemoprotein of NADPH sulfite reductase;
- cc) the *cysH* gene coding for adenylyl sulfate reductase;
- dd) the *phoB* gene coding for the positive regulator PhoB of the *pho* regulon;
- ee) the *phoR* gene coding for the sensor protein of the *pho* regulon;
- ff) the *phoE* gene coding for protein E of the outer cell membrane;
- gg) the *pykF* gene coding for pyruvate kinase I, which is stimulated by fructose;
- hh) the *pfkB* gene coding for 6-phosphofructokinase II;
- ii) the *malE* gene coding for the periplasmic binding protein of maltose transport;
- jj) the *sodA* gene coding for superoxide dismutase;
- kk) the *rseA* gene coding for a membrane protein with anti- σ^E activity;
- ll) the *rseC* gene coding for a global regulator of the σ^E factor;
- mm) the *sucA* gene coding for the decarboxylase subunit of 2-ketoglutarate dehydrogenase;
- nn) the *sucB* gene coding for the dihydrolipoyl transsuccinase E2 subunit of 2-ketoglutarate dehydrogenase;
- oo) the *sucC* gene coding for the β -subunit of succinyl-CoA synthetase;
- pp) the *sucD* gene coding for the α -subunit of succinyl-CoA synthetase;
- qq) the *adk* gene coding for adenylate kinase;
- rr) the *hdeA* gene coding for a periplasmic protein with chaperonin-type function;
- ss) the *hdeB* gene coding for a periplasmic protein with chaperonin-type function;
- tt) the *icd* gene coding for isocitrate dehydrogenase;
- uu) the *mglB* gene coding for the periplasmic, galactose-binding transport protein;
- vv) the *lpd* gene coding for dihydrolipoamide dehydrogenase;
- ww) the *aceE* gene coding for the E1 component of the pyruvate-dehydrogenase complex;

- xx) the *aceF* gene coding for the E2 component of the pyruvate-dehydrogenase complex;
 - yy) the *pepB* gene coding for aminopeptidase B;
 - zz) the *aldH* gene coding for aldehyde dehydrogenase,
 - aaa) the *bfr* gene coding for the iron-storage homoprotein;
 - bbb) the *udp* gene coding for uridine phosphorylase; and
 - ccc) the *rseB* gene coding for the regulator of sigmaE-factor activity.
28. (New) The process of claim 21, wherein said L-amino acid is selected from the group consisting of: L-threonine; L-lysine; L-isoleucine, L-valine, L-methionine, and L-homoserine.
29. (New) The process of claim 21, wherein said L-amino acid is either L-threonine or L-lysine.
30. (New) The process of claim 28, wherein said ORF encodes protein that consists of the amino acid sequence of SEQ ID NO:4
31. (New) The process of claim 28, wherein some or all of the constituents of said fermentation medium and/or the biomass of said recombinant microorganism are isolated with said L-amino acid.
32. (New) The process of claim 28, wherein said ORF that encodes a protein with the amino acid sequence of SEQ ID NO:4 comprises the nucleotide sequence of SEQ ID NO:3.
33. (New) The process of claim 32 wherein said ORF that encodes a protein with the amino acid sequence of SEQ ID NO:4 consists of the nucleotide sequence of SEQ ID NO:3.

34. (New) The process of claim 28, wherein the genus of said recombinant microorganism is selected from the group consisting of: *Escherichia*; *Erwinia*; *Providencia*; and *Serratia*.
35. (New) The process of claim 28, wherein said microorganism overexpresses said ORF and, in addition, the activity of one or more additional genes is overexpressed, said one or more additional genes being selected from the group consisting of:
- a) the thrABC operon coding for aspartate kinase, homoserine dehydrogenase, homoserine kinase and threonine synthase;
 - b) the pyc gene coding for pyruvate carboxylase;
 - c) the pps gene for phosphoenolpyruvate synthase;
 - d) the ppc gene coding for phosphoenolpyruvate carboxylase;
 - e) the genes pntA and pntB coding for transhydrogenase;
 - f) the rhtB gene imparting homoserine resistance;
 - g) the mqo gene coding for malate:quinone oxidoreductase;
 - h) the rhtC gene imparting threonine resistance;
 - i) the thrE gene coding for the threonine-export protein;
 - j) the gdhA gene coding for glutamate dehydrogenase;
 - k) the hns gene coding for the DNA binding protein HLP-II;
 - l) the pgm gene coding for phosphoglucomutase;
 - m) the fba gene coding for fructose biphosphate aldolase;
 - n) the ptsH gene coding for phosphohistidine protein hexosé phosphotransferase;
 - o) the ptsI gene coding for enzyme I of the phosphotransferase system;
 - p) the crr gene coding for the glucose-specific IIA component;
 - q) the ptsG gene coding for the glucose-specific IIBC component;
 - r) the lrp gene coding for the regulator of the leucine regulon;
 - s) the csrA gene coding for the global regulator Csr;
 - t) the fadR gene coding for the regulator of the fad regulon;
 - u) the iclR gene coding for the regulator of central intermediary metabolism;
 - v) the mopB gene coding for the 10 kDa chaperon;
 - w) the ahpC gene coding for the small subunit of alkyl hydroperoxide reductase;
 - x) the ahpF gene coding for the large subunit of alkyl hydroperoxide reductase;

- y) the *cysK* gene coding for cysteine synthase A;
- z) the *cysB* gene coding for the regulator of the *cys* regulon;
- aa) the *cysJ* gene coding for the flavoprotein of NADPH sulfite reductase;
- bb) the *cysI* gene coding for the haemoprotein of NADPH sulfite reductase;
- cc) the *cysH* gene coding for adenylyl sulfate reductase;
- dd) the *phoB* gene coding for the positive regulator PhoB of the *pho* regulon;
- ee) the *phoR* gene coding for the sensor protein of the *pho* regulon;
- ff) the *phoE* gene coding for protein E of the outer cell membrane;
- gg) the *pykF* gene coding for pyruvate kinase I, which is stimulated by fructose;
- hh) the *pfkB* gene coding for 6-phosphofructokinase II;
- ii) the *malE* gene coding for the periplasmic binding protein of maltose transport;
- jj) the *sodA* gene coding for superoxide dismutase;
- kk) the *rseA* gene coding for a membrane protein with anti- σ^E activity;
- ll) the *rseC* gene coding for a global regulator of the σ^E factor;
- mm) the *sucA* gene coding for the decarboxylase subunit of 2-ketoglutarate dehydrogenase;
- nn) the *sucB* gene coding for the dihydrolipoyl transsuccinase E2 subunit of 2-ketoglutarate dehydrogenase;
- oo) the *sucC* gene coding for the β -subunit of succinyl-CoA synthetase;
- pp) the *sucD* gene coding for the α -subunit of succinyl-CoA synthetase;
- qq) the *adk* gene coding for adenylate kinase;
- rr) the *hdeA* gene coding for a periplasmic protein with chaperonin-type function;
- ss) the *hdeB* gene coding for a periplasmic protein with chaperonin-type function;
- tt) the *icd* gene coding for isocitrate dehydrogenase;
- uu) the *mglB* gene coding for the periplasmic, galactose-binding transport protein;
- vv) the *lpd* gene coding for dihydrolipoamide dehydrogenase;
- ww) the *aceE* gene coding for the E1 component of the pyruvate-dehydrogenase complex;
- xx) the *aceF* gene coding for the E2 component of the pyruvate-dehydrogenase complex;
- yy) the *pepB* gene coding for aminopeptidase B;
- zz) the *aldH* gene coding for aldehyde dehydrogenase,

- aaa) the bfr gene coding for the iron-storage homoprotein;
- bbb) the udp gene coding for uridine phosphorylase; and
- ccc) the rseB gene coding for the regulator of sigmaE-factor activity.